

SEQUENCE LISTING

<110> Olmsted, Robert
Keith, Paula
Dryga, Sergey
Caley, Ian
Maughan, Maureen
Johnston, Robert
Davis, Nancy
Swanstrom, Ronald

<120> ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE AS
VACCINES

<130> 01113.0001U3

<150> 09/902,537

<151> 2001-07-09

<150> 60/216,995

<151> 2000-07-07

<160> 19

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence; Note =
synthetic construct

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<223> Description of Artificial Sequence; Note =
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<221> CDS
<222> (1) ... (7479)

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Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser
      35             40             45

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Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile
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Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys
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6
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Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu	
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Glu Thr Glu Thr Met Cys Leu His Asp Asp Glu Ser Cys Arg Tyr Glu	
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Ser Leu Tyr His Gln Ala Asn Lys Gly Val Arg Val Ala Tyr Trp Ile	
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Asn Ile Gly Leu Cys Ser Ser Asp Val Met Glu Arg Ser Arg Arg Gly	
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Ser Trp His Leu Pro Ser Val Phe His Leu Arg Gly Lys Gln Asn Tyr	
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Thr Cys Arg Cys Glu Thr Ile Val Ser Cys Asp Gly Tyr Val Val Lys	
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Arg Ile Ala Ile Ser Pro Gly Leu Tyr Gly Lys Pro Ser Gly Tyr Ala	
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Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu Leu	
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Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu	
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1460 1465 1470	
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Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg	
1475 1480 1485	
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Gly Val Gln Lys Ile Gln Cys Ser Gln Pro Ile Leu Phe Ser Pro Lys	
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Val Pro Ala Tyr Ile His Pro Arg Lys Tyr Leu Val Glu Thr Pro Pro	
1650 1655 1660	

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gcg ttc gta gca caa caa caa tga cgg ttt gat gcg ggt gca tac atc 5664
Ala Phe Val Ala Gln Gln Gln * Arg Phe Asp Ala Gly Ala Tyr Ile
1875 1880 1885

Figure 1 consists of 12 bar charts arranged in a 3x4 grid. Each chart displays the percentage of respondents for a specific demographic or marital category across six age groups: 18-24, 25-34, 35-44, 45-54, 55-64, and 65+. The y-axis for all charts ranges from 0 to 100. The categories are: 1. Total respondents, 2. Male respondents, 3. Female respondents, 4. White respondents, 5. Black respondents, 6. Hispanic respondents, 7. Asian respondents, 8. Other respondents, 9. Married respondents, 10. Single respondents, 11. Divorced respondents, and 12. Widowed respondents. The data is represented by horizontal bars for each age group, with the percentage value labeled at the end of each bar.

Category	18-24	25-34	35-44	45-54	55-64	65+
1. Total respondents	100	100	100	100	100	100
2. Male respondents	50	50	50	50	50	50
3. Female respondents	50	50	50	50	50	50
4. White respondents	75	75	75	75	75	75
5. Black respondents	15	15	15	15	15	15
6. Hispanic respondents	5	5	5	5	5	5
7. Asian respondents	2	2	2	2	2	2
8. Other respondents	1	1	1	1	1	1
9. Married respondents	65	65	65	65	65	65
10. Single respondents	35	35	35	35	35	35
11. Divorced respondents	10	10	10	10	10	10
12. Widowed respondents	1	1	1	1	1	1

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1890 1895 1900	
caa acg gtg cta tcc gaa gtg gtg ttg gag agg acc gaa ttg gag att	5760
Gln Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile	
1905 1910 1915	
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Ser Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys	
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1955 1960 1965	
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Gly Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg	
1970 1975 1980	
acc ctg cat cct gtt cct ttg tat tca tct agt gtg aac cgt gcc ttt	6000
Thr Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe	
1985 1990 1995	
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Ser Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu	
2000 2005 2010 2015	
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Asn Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala	
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Tyr Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser	
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Phe Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu	
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Glu Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu	
2065 2070 2075	
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Gln Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln	
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2115 2120 2125	

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Asn Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys	
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Leu Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu	
2145 2150 2155	
aat atg ttg cag gac ata cca atg gac agg ttt gta atg gac tta aag	6528
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2160 2165 2170 2175	
aga gac gtg aaa gtg act cca gga aca aaa cat act gaa gaa cgg ccc	6576
Arg Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro	
2180 2185 2190	
aag gta cag gtg atc cag gct gcc gat ccg cta gca aca gcg tat ctg	6624
Lys Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu	
2195 2200 2205	
tgc gga atc cac cga gag ctg gtt agg aga tta aat gcg gtc ctg ctt	6672
Cys Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu	
2210 2215 2220	
ccg aac att cat aca ctg ttt gat atg tcg gct gaa gac ttt gac gct	6720
Pro Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala	
2225 2230 2235	
att ata gcc gag cac ttc cag cct ggg gat tgt gtt ctg gaa act gac	6768
Ile Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp	
2240 2245 2250 2255	
atc gcg tcg ttt gat aaa agt gag gac gac gcc atg gct ctg acc gcg	6816
Ile Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala	
2260 2265 2270	
tta atg att ctg gaa gac tta ggt gtg gac gca gag ctg ttg acg ctg	6864
Leu Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu	
2275 2280 2285	
att gag gcg gct ttc ggc gaa att tca tca ata cat ttg ccc act aaa	6912
Ile Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys	
2290 2295 2300	
act aaa ttt aaa ttc gga gcc atg atg aaa tct gga atg ttc ctc aca	6960
Thr Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr	
2305 2310 2315	
ctg ttt gtg aac aca gtc att aac att gta atc gca agc aga gtg ttg	7008
Leu Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu	
2320 2325 2330 2335	
aga gaa cgg cta acc gga tca cca tgt gca gca ttc att gga gat gac	7056
Arg Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp	
2340 2345 2350	
aat atc gtg aaa gga gtc aaa tcg gac aaa tta atg gca gac agg tgc	7104
Asn Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys	
2355 2360 2365	

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10:31:14

gcc acc tgg ttg aat atg gaa gtc aag att ata gat gct gtg gtg ggc 7152
 Ala Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly
 2370 2375 2380

gag aaa gcg ccc tat ttc tgt gga ggg ttt att ttg tgt gac tcc gtg 7200
 Glu Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val
 2385 2390 2395

acc ggc aca gcg tgc cgt gtg gca gac ccc cta aaa agg ctg ttt aag 7248
 Thr Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys
 2400 2405 2410 2415

ctt ggc aaa cct ctg gca gca gac gat gaa cat gat gat gac agg aga 7296
 Leu Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg
 2420 2425 2430

agg gca ttg cat gaa gag tca aca cgc tgg aac cga gtg ggt att ctt 7344
 Arg Ala Leu His Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu
 2435 2440 2445

tca gag ctg tgc aag gca gta gaa tca agg tat gaa acc gta gga act 7392
 Ser Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr
 2450 2455 2460

tcc atc ata gtt atg gcc atg act act cta gct agc agt gtt aaa tca 7440
 Ser Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser
 2465 2470 2475

ttc agc tac ctg aga ggg gcc cct ata act ctc tac ggc 7479
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<211> 2492

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
 synthetic construct

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 Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser
 35 40 45
 Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile
 50 55 60
 Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys
 65 70 75 80
 Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr
 85 90 95
 Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu
 100 105 110

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 16

Asp	Lys	Lys	Met	Lys	Glu	Leu	Ala	Ala	Val	Met	Ser	Asp	Pro	Asp	Leu
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Glu	Thr	Glu	Thr	Met	Cys	Leu	His	Asp	Asp	Glu	Ser	Cys	Arg	Tyr	Glu
	130					135					140				
Gly	Gln	Val	Ala	Val	Tyr	Gln	Asp	Val	Tyr	Ala	Val	Asp	Gly	Pro	Thr
145					150					155					160
Ser	Leu	Tyr	His	Gln	Ala	Asn	Lys	Gly	Val	Arg	Val	Ala	Tyr	Trp	Ile
				165					170					175	
Gly	Phe	Asp	Thr	Thr	Pro	Phe	Met	Phe	Lys	Asn	Leu	Ala	Gly	Ala	Tyr
			180					185					190		
Pro	Ser	Tyr	Ser	Thr	Asn	Trp	Ala	Asp	Glu	Thr	Val	Leu	Thr	Ala	Arg
		195					200					205			
Asn	Ile	Gly	Leu	Cys	Ser	Ser	Asp	Val	Met	Glu	Arg	Ser	Arg	Arg	Gly
210						215					220				
Met	Ser	Ile	Leu	Arg	Lys	Lys	Tyr	Leu	Lys	Pro	Ser	Asn	Asn	Val	Leu
225					230					235					240
Phe	Ser	Val	Gly	Ser	Thr	Ile	Tyr	His	Glu	Lys	Arg	Asp	Leu	Leu	Arg
				245					250					255	
Ser	Trp	His	Leu	Pro	Ser	Val	Phe	His	Leu	Arg	Gly	Lys	Gln	Asn	Tyr
			260				265						270		
Thr	Cys	Arg	Cys	Glu	Thr	Ile	Val	Ser	Cys	Asp	Gly	Tyr	Val	Val	Lys
		275				280						285			
Arg	Ile	Ala	Ile	Ser	Pro	Gly	Leu	Tyr	Gly	Lys	Pro	Ser	Gly	Tyr	Ala
290						295					300				
Ala	Thr	Met	His	Arg	Glu	Gly	Phe	Leu	Cys	Cys	Lys	Val	Thr	Asp	Thr
305					310					315					320
Leu	Asn	Gly	Glu	Arg	Val	Ser	Phe	Pro	Val	Cys	Thr	Tyr	Val	Pro	Ala
				325					330					335	
Thr	Leu	Cys	Asp	Gln	Met	Thr	Gly	Ile	Leu	Ala	Thr	Asp	Val	Ser	Ala
			340				345						350		
Asp	Asp	Ala	Gln	Lys	Leu	Leu	Val	Gly	Leu	Asn	Gln	Arg	Ile	Val	Val
		355					360					365			
Asn	Gly	Arg	Thr	Gln	Arg	Asn	Thr	Asn	Thr	Met	Lys	Asn	Tyr	Leu	Leu
370						375					380				
Pro	Val	Val	Ala	Gln	Ala	Phe	Ala	Arg	Trp	Ala	Lys	Glu	Tyr	Lys	Glu
385					390					395					400
Asp	Gln	Glu	Asp	Glu	Arg	Pro	Leu	Gly	Leu	Arg	Asp	Arg	Gln	Leu	Val
				405					410					415	
Met	Gly	Cys	Cys	Trp	Ala	Phe	Arg	Arg	His	Lys	Ile	Thr	Ser	Ile	Tyr
			420				425					430			
Lys	Arg	Pro	Asp	Thr	Gln	Thr	Ile	Ile	Lys	Val	Asn	Ser	Asp	Phe	His
		435					440					445			
Ser	Phe	Val	Leu	Pro	Arg	Ile	Gly	Ser	Asn	Thr	Leu	Glu	Ile	Gly	Leu
450						455					460				
Arg	Thr	Arg	Ile	Arg	Lys	Met	Leu	Glu	Glu	His	Lys	Glu	Pro	Ser	Pro
465					470					475					480
Leu	Ile	Thr	Ala	Glu	Asp	Val	Gln	Glu	Ala	Lys	Cys	Ala	Ala	Asp	Glu
				485					490					495	
Ala	Lys	Glu	Val	Arg	Glu	Ala	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Pro	Pro
			500				505					510			
Leu	Ala	Ala	Asp	Val	Glu	Glu	Pro	Thr	Leu	Glu	Ala	Asp	Val	Asp	Leu
		515					520					525			
Met	Leu	Gln	Glu	Ala	Gly	Ala	Gly	Ser	Val	Glu	Thr	Pro	Arg	Gly	Leu
					530		535				540				
Ile	Lys	Val	Thr	Ser	Tyr	Ala	Gly	Glu	Asp	Lys	Ile	Gly	Ser	Tyr	Ala
545					550					555					560

00001253 "11601

Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile
 565 570 575
 His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys
 580 585 590
 Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu
 595 600 605
 Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala
 610 615 620
 Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His
 625 630 635 640
 Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys
 645 650 655
 Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp
 660 665 670
 Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr
 675 680 685
 Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu
 690 695 700
 Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr
 705 710 715 720
 Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr
 725 730 735
 Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile
 740 745 750
 Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr
 755 760 765
 Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu
 770 775 780
 Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu
 785 790 795 800
 Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys
 805 810 815
 Gln Cys Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His
 820 825 830

 Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr
 835 840 845
 Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met
 850 855 860
 Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly
 865 870 875 880
 Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly
 885 890 895
 Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr
 900 905 910
 Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg
 915 920 925
 Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val
 930 935 940
 Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu
 945 950 955 960
 Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn
 965 970 975
 Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met
 980 985 990

0591253
 44604

[illegible]

1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu
 1860 1865 1870
 Ala Phe Val Ala Gln Gln Gln Arg Phe Asp Ala Gly Ala Tyr Ile Phe
 1875 1880 1885
 Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg Gln
 1890 1895 1900
 Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile Ser
 1905 1910 1915 1920
 Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys Lys
 1925 1930 1935
 Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser Arg
 1940 1945 1950
 Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln Gly
 1955 1960 1965
 Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg Thr
 1970 1975 1980
 Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe Ser
 1985 1990 1995 2000
 Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu Asn
 2005 2010 2015
 Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala Tyr
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 Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser Phe
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 Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu Gln
 2065 2070 2075 2080
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 2145 2150 2155 2160
 Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys Arg
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 2180 2185 2190
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 2195 2200 2205
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 Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile
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 Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp Ile
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 Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu Ile
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 Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu
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 2370 2375 2380
 Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val Thr
 2385 2390 2395 2400
 Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu
 2405 2410 2415
 Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg Arg
 2420 2425 2430
 Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu Ser
 2435 2440 2445
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<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
synthetic construct

<221> CDS

<222> (1)...(1476)

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gaa aag att agg tta agg cca ggg gga aag aaa cat tat atg tta aaa	96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys	
20 25 30	
cac ata gta tgg gcg agc agg gag ctg gaa aga ttt gca ctt aac cct	144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro	
35 40 45	
ggc ctt tta gaa aca tca gaa gga tgt aaa caa ata atg aaa cag cta	192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu	
50 55 60	

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caa cca gct ctc cag aca gga aca gag gaa ctt aaa tca tta tac aac	240
Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn	
65 70 75 80	
aca gta gca act ctc tat tgt gta cat gaa aag ata gaa gta cga gac	288
Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp	
85 90 95	
acc aag gaa gcc tta gat aag ata gag gaa gaa caa aac aaa tgt cag	336
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln	
100 105 110	
caa aaa acg cag cag gca aaa gcg gct gac ggg aaa gtc agt caa aat	384
Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn	
115 120 125	
tat cct ata gtg cag aat ctc caa ggg caa atg gta cat caa gcc ata	432
Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile	
130 135 140	
tca cct aga acc ttg aat gca tgg gta aaa gta ata gaa gaa aag gct	480
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala	
145 150 155 160	
ttt agc cca gag gta ata ccc atg ttt aca gca tta tca gaa gga gcc	528
Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala	
165 170 175	
acc cca caa gat tta aac acc atg tta aat aca gtg ggg gga cac caa	576
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
180 185 190	
gca gcc atg caa atg tta aaa gat act att aat gaa gag gct gca gaa	624
Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu	
195 200 205	
tgg gat aga tta cat cca gtc cat gcg ggg cct att gca cca ggc cag	672
Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln	
210 215 220	
atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt	720
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu	
225 230 235 240	
cag gaa caa ata gca tgg atg aca agt aac cca cct att cca gtg gga	768
Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly	
245 250 255	
gac atc tat aaa aga tgg ata att ctg ggg tta aat aaa ata gtg aga	816
Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg	
260 265 270	
atg tat agc ccg gtc agc att ttg gac ata aga caa ggg cca aag gaa	864
Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu	
275 280 285	

059158 1160

ccc ttt cga gac tat gta gat cgg ttc ttt aaa act tta aga gct gaa 912
 Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
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caa gct aca caa gaa gta aaa aat tgg atg aca gac acc ttg tta gtc 960
 Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
 305 310 315 320

caa aat gcg aac cca gat tgt aag acc att ttg aga gca tta gga cca 1008
 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
 325 330 335

ggg gct aca tta gaa gaa atg atg aca gca tgt caa ggg gtg gga gga 1056
 Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
 340 345 350

cct ggc cac aaa gca aga gta ttg gct gag gca atg agt caa aca aac 1104
 Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
 355 360 365

agt gga aac ata atg atg cag aga agc aat ttt aaa ggc cct aga aga 1152
 Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg
 370 375 380

att gtt aaa tgt ttt aac tgt ggc aag gaa ggg cac ata gcc aga aat 1200
 Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
 385 390 395 400

tgc aga gcc cct agg aaa aaa ggc tgt tgg aaa tgt gga aaa gaa gga 1248
 Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
 405 410 415

cac caa atg aaa gac tgc act gag agg cag gct aat ttt tta ggg aaa 1296
 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
 420 425 430

att tgg cct tcc cac aag ggg agg cca ggg aat ttc ctt cag aac aga 1344
 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
 435 440 445

cca gag cca aca gcc cca cca gca gag agc ttc agg ttc gaa gag aca 1392
 Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
 450 455 460

acc ccc gct ccg aaa cag gag ccg ata gaa agg gaa ccc tta act tcc 1440
 Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser
 465 470 475 480

ctc aaa tca ctc ttt ggc agc gac ccc ttg tct caa 1476
 Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln
 485 490

<210> 5

<211> 492

<212> PRT

<213> Artificial Sequence

0991551.1
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<223> Description of Artificial Sequence; Note =
synthetic construct

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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	His	Tyr	Met	Leu	Lys
			20					25					30		
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Leu	Asn	Pro
		35					40					45			
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Lys	Gln	Ile	Met	Lys	Gln	Leu
	50					55					60				
Gln	Pro	Ala	Leu	Gln	Thr	Gly	Thr	Glu	Glu	Leu	Lys	Ser	Leu	Tyr	Asn
65					70				75					80	
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Glu	Lys	Ile	Glu	Val	Arg	Asp
				85					90					95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Cys	Gln
			100					105					110		
Gln	Lys	Thr	Gln	Gln	Ala	Lys	Ala	Ala	Asp	Gly	Lys	Val	Ser	Gln	Asn
		115					120					125			
Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile
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Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Ile	Glu	Glu	Lys	Ala
145					150					155					160
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Thr	Ala	Leu	Ser	Glu	Gly	Ala
				165					170					175	
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln
			180					185					190		
Ala	Ala	Met	Gln	Met	Leu	Lys	Asp	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu
		195					200					205			
Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln
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Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu
225					230					235					240
Gln	Glu	Gln	Ile	Ala	Trp	Met	Thr	Ser	Asn	Pro	Pro	Ile	Pro	Val	Gly
				245					250					255	
Asp	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg
			260					265					270		
Met	Tyr	Ser	Pro	Val	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu
		275					280					285			
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Phe	Lys	Thr	Leu	Arg	Ala	Glu
	290					295					300				
Gln	Ala	Thr	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Asp	Thr	Leu	Leu	Val
305					310					315					320
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Arg	Ala	Leu	Gly	Pro
				325					330					335	
Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
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Pro	Gly	His	Lys	Ala	Arg										

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<210> 6
<211> 813
<212> DNA
<213> Artificial Sequence
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<221> CDS
<222> (1) ... (813)
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1				5					10					15		
tcc	aac	atg	gat	gct	gat	tta	tat	ggg	tat	aaa	tgg	gct	cgc	gat	aat	96
Ser	Asn	Met	Asp	Ala	Asp	Leu	Tyr	Gly	Tyr	Lys	Trp	Ala	Arg	Asp	Asn	
			20					25					30			
gtc	ggg	caa	tca	ggt	gcg	aca	atc	tat	cga	ttg	tat	ggg	aag	ccc	gat	144
Val	Gly	Gln	Ser	Gly	Ala	Thr	Ile	Tyr	Arg	Leu	Tyr	Gly	Lys	Pro	Asp	
		35					40					45				
gcg	cca	gag	ttg	ttt	ctg	aaa	cat	ggc	aaa	ggg	agc	gtt	gcc	aat	gat	192
Ala	Pro	Glu	Leu	Phe	Leu	Lys	His	Gly	Lys	Gly	Ser	Val	Ala	Asn	Asp	
	50					55					60					
gtt	aca	gat	gag	atg	gtc	aga	cta	aac	tgg	ctg	acg	gaa	ttt	atg	cct	240
Val	Thr	Asp	Glu	Met	Val	Arg	Leu	Asn	Trp	Leu	Thr	Glu	Phe	Met	Pro	
65					70				75					80		
ctt	ccg	acc	atc	aag	cat	ttt	atc	cgt	act	cct	gat	gat	gca	tgg	tta	288
Leu	Pro	Thr	Ile	Lys	His	Phe	Ile	Arg	Thr	Pro	Asp	Asp	Ala	Trp	Leu	
				85					90					95		
ctc	acc	act	gcg	atc	ccc	ggg	aaa	aca	gca	ttc	cag	gta	tta	gaa	gaa	336
Leu	Thr	Thr	Ala	Ile	Pro	Gly	Lys	Thr	Ala	Phe	Gln	Val	Leu	Glu	Glu	
			100					105					110			

Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn
1 5 10 15
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn
20 25 30

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp
 35 40 45
 Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp
 50 55 60
 Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro
 65 70 75 80
 Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu
 85 90 95
 Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu
 100 105 110
 Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu
 115 120 125
 Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp
 130 135 140
 Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu
 145 150 155 160
 Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu
 165 170 175
 Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser
 180 185 190
 Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu
 195 200 205
 Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp
 210 215 220
 Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser
 225 230 235 240
 Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro
 245 250 255
 Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe
 260 265 270

<210> 8

<211> 5076

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
 synthetic construct

<400> 8

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<210> 9

<211> 1026

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
synthetic construct

<221> CDS

<222> (1)...(1026)

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aac ccg ttc gcg gcc ccg cgc agg ccc tgg ttc ccc aga acc gac cct	96
Asn Pro Phe Ala Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro	
20 25 30	
ttt ctg gcg atg cag gtg cag gaa tta acc cgc tcg atg gct aac ctg	144
Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu	
35 40 45	
acg ttc aag caa cgc cgg gac gcg cca cct gag ggg cca tcc gct aag	192
Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys	
50 55 60	
aaa ccg aag aag gag gcc tcg caa aaa cag aaa ggg gga ggc caa ggg	240
Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly	
65 70 75 80	
aag aag aag aag aac caa ggg aag aag aag gct aag aca ggg ccg cct	288
Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro	
85 90 95	

1091650

aat ccg aag gca cag aat gga aac aag aag aag acc aac aag aaa cca	336
Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro	
100 105 110	
ggc aag aga cag cgc atg gtc atg aaa ttg gaa tct gac aag acg ttc	384
Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe	
115 120 125	
cca atc atg ttg gaa ggg aag ata aac ggc tac gct tgt gtg gtc gga	432
Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly	
130 135 140	
ggg aag tta ttc agg ccg atg cat gtg gaa ggc aag atc gac aac gac	480
Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp	
145 150 155 160	
gtt ctg gcc gcg ctt aag acg aag aaa gca tcc aaa tac gat ctt gag	528
Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu	
165 170 175	
tat gca gat gtg cca cag aac atg cgg gcc gat aca ttc aaa tac acc	576
Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr	
180 185 190	
cat gag aaa ccc caa ggc tat tac agc tgg cat cat gga gca gtc caa	624
His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln	
195 200 205	
tat gaa aat ggg cgt ttc acg gtg ccg aaa gga gtt ggg gcc aag gga	672
Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly	
210 215 220	
gac agc gga cga ccc att ctg gat aac cag gga cgg gtg gtc gct att	720
Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile	
225 230 235 240	
gtg ctg gga ggt gtg aat gaa gga tct agg aca gcc ctt tca gtc gtc	768
Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val	
245 250 255	
atg tgg aac gag aag gga gtt acc gtg aag tat act ccg gag aac tgc	816
Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys	
260 265 270	
gag caa tgg tca cta gtg acc acc atg tgt ctg ctc gcc aat gtg acg	864
Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr	
275 280 285	
ttc cca tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag	912
Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu	
290 295 300	
act ttg gcc atg ctc agc gtt aac atc cct gct ggg agg atc agc cgt	960
Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg	
305 310 315 320	

aat tat tat aat tgg ctt ggt gct ggc tac tat tgt ggc cat gta cgt 1008
 Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg
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gct gac caa cca gaa aca 1026
 Ala Asp Gln Pro Glu Thr
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<210> 10

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
 synthetic construct

<400> 10

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 20 25 30
 Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu
 35 40 45
 Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys
 50 55 60
 Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly
 65 70 75 80
 Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro
 85 90 95
 Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro
 100 105 110
 Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe
 115 120 125
 Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly
 130 135 140
 Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp
 145 150 155 160
 Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu
 165 170 175
 Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr
 180 185 190
 His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln
 195 200 205
 Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly
 210 215 220
 Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile
 225 230 235 240
 Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val
 245 250 255
 Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys
 260 265 270
 Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr
 275 280 285

"EST" 11601

[illegible]

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<210> 12

<211> 2943

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
synthetic construct

<221> CDS

<222> (1)...(2943)

<400> 12

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1 5 10 15

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tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag act ttg 96
Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu
20 25 30

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gcc atg ctc agc gtt aac gtt gac aac ccg ggc tac gat gag ctg ctg 144
Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu
35 40 45

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gaa gca gct gtt aag tgc ccc gga agg aaa agg aga tcc acc gag gag 192
Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu
50 55 60

```

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ctg ttt aag gag tat aag cta acg cgc cct tac atg gcc aga tgc atc 240
Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile
65 70 75 80

```

aga tgt gca gtt ggg agc tgc cat agt cca ata gca atc gag gca gta	288
Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val	
85 90 95	
aag agc gac ggg cac gac ggt tat gtt aga ctt cag act tcc tcg cag	336
Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln	
100 105 110	
tat ggc ctg gat tcc tcc ggc aac tta aag ggc agg acc atg cgg tat	384
Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr	
115 120 125	
gac atg cac ggg acc att aaa gag ata cca cta cat caa gtg tca ctc	432
Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu	
130 135 140	
cat aca tct cgc ccg tgt cac att gtg gat ggg cac ggt tat ttc ctg	480
His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu	
145 150 155 160	
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Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys	
165 170 175	
gat tcc gtc aca cac tcc tgc tcg gtg ccg tat gaa gtg aaa ttt aat	576
Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn	
180 185 190	
cct gta ggc aga gaa ctc tat act cat ccc cca gaa cac gga gta gag	624
Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu	
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Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr	
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Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser	
225 230 235 240	
ttg agc ggc agt tca gtc acc gtg aca cct cct gtt ggg act agc gcc	768
Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala	
245 250 255	
ctg gtg gaa tgc gag tgt ggc ggc aca aag atc tcc aag acc atc aac	816
Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn	
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aag aca aaa cag ttc agc cag tgc aca aag aag gag cag tgc aga gca	864
Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala	
275 280 285	
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Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro	
290 295 300	

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Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile	
325 330 335	
acc ttc ggt ttc aga tca gtg tca ctg aaa ctg cac cct aag aat ccc	1056
Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro	
340 345 350	
aca tat cta acc acc cgc caa ctt gct gat gag cct cac tac acg cat	1104
Thr Tyr Leu Thr Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His	
355 360 365	
gag ctc ata tct gaa cca gct gtt agg aat ttt acc gtc acc gga aaa	1152
Glu Leu Ile Ser Glu Pro Ala Val Arg Asn Phe Thr Val Thr Gly Lys	
370 375 380	
ggg tgg gag ttt gta tgg gga aac cac ccg ccg aaa agg ttt tgg gca	1200
Gly Trp Glu Phe Val Trp Gly Asn His Pro Pro Lys Arg Phe Trp Ala	
385 390 395 400	
cag gaa aca gca ccc gga aat cca cat ggg cta ccg cac gag gtg ata	1248
Gln Glu Thr Ala Pro Gly Asn Pro His Gly Leu Pro His Glu Val Ile	
405 410 415	
act cat tat tac cac aga tac cct atg tcc acc atc ctg ggt ttg tca	1296
Thr His Tyr Tyr His Arg Tyr Pro Met Ser Thr Ile Leu Gly Leu Ser	
420 425 430	
att tgt gcc gcc att gca acc gtt tcc gtt gca gcg tct acc tgg ctg	1344
Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu	
435 440 445	
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Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro	
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Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr	
465 470 475 480	
gcc cgg gcc gag acc acc tgg gag tcc ttg gat cac cta tgg aac aat	1488
Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn	
485 490 495	
aac caa cag atg ttc tgg att caa ttg ctg atc cct ctg gcc gcc ttg	1536
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Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe	
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Thr Met Pro Ser Gln Ala Gly Ile Ser Tyr Asn Thr Ile Val Asn Arg
545 550 555 560

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Leu Ile Pro Thr Val Asn Leu Glu Tyr Val Thr Cys His Tyr Lys Thr
580 585 590

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Pro Thr Tyr Arg Pro Asp Glu Gln Cys Lys Val Phe Thr Gly Val Tyr
610 615 620

caa gtc agc aag gcc tac gta atg aaa tct gac gac tgc ctt gcg gat 1968
Gln Val Ser Lys Ala Tyr Val Met Lys Ser Asp Asp Cys Leu Ala Asp
645 650 655

aac atc aca gtg gga gaa cac tct att gtg act acc gtg tat gtg aat 2064
Asn Ile Thr Val Gly Glu His Ser Ile Val Thr Thr Val Tyr Val Asn
675 680 685

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Leu Ser Thr Ala Trp Thr Pro Phe Asp Arg Lys Ile Val Gln Tyr Ala
705 710 715 720

gga gca ttt gga gat ata caa tcc aga aca gtc tca agc tca gat ctg 2256
Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu
740 745 750

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Depression score	0.4	0.4	0	1
Life satisfaction	0.6	0.3	0	1
Work satisfaction	0.5	0.4	0	1
Family satisfaction	0.6	0.3	0	1
Overall well-being	0.5	0.3	0	1

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755 760 765	
cac gtg cca tac act cag gca cct tcg ggt ttt gag caa tgg aag aaa	2352
His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys	
770 775 780	
gat aaa gct cca tca ttg aaa ttt acc gcc cct ttc gga tgc gaa ata	2400
Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile	
785 790 795 800	
tat aca aac ccc att cgc gcc gaa aac tgt act gta ggg tca att cca	2448
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Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser	
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885 890 895	
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Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr	
915 920 925	
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His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr	
930 935 940	
gcg tgg acg tgg tta aca tcc ctg ctg gga gga tca gcc gta att att	2880
Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile	
945 950 955 960	
ata att ggc ttg gtg ctg gct act att gtg gcc atg tac gtg ctg acc	2928
Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr	
965 970 975	

099433-11601

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 Asn Gln Lys His Asn
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2943

<210> 13
 <211> 981
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 synthetic construct

<400> 13

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Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
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<211> 1323

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence; Note =
synthetic construct

<221> CDS

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Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile
      50             55             60

aaa aag gaa gac agc act aag tgg aga aaa tta gta gat ttc agg gaa     240
Lys Lys Glu Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu
      65             70             75             80

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Variable	Control group		Experimental group		P value
	Mean	SD	Mean	SD	
Age (years)	38.5	10.2	39.1	11.5	0.85
Weight (kg)	72.5	12.1	71.8	13.4	0.92
Height (cm)	175.2	5.8	174.9	6.2	0.78
Preoperative hemoglobin (g/dL)	13.2	1.5	13.1	1.6	0.95
Preoperative hematocrit (%)	39.5	4.2	39.2	4.5	0.88
Preoperative serum ferritin (ng/mL)	125	45	128	52	0.72
Preoperative serum transferrin saturation (%)	28.5	5.1	28.2	5.5	0.81
Preoperative serum ferritin (ng/mL)	125	45	128	52	0.72
Preoperative serum transferrin saturation (%)	28.5	5.1	28.2	5.5	0.81
Postoperative hemoglobin (g/dL)	12.8	1.4	12.9	1.5	0.91
Postoperative hematocrit (%)	38.2	4.1	38.5	4.4	0.89
Postoperative serum ferritin (ng/mL)	132	48	135	55	0.75
Postoperative serum transferrin saturation (%)	29.1	5.3	29.4	5.7	0.83
Postoperative serum ferritin (ng/mL)	132	48	135	55	0.75
Postoperative serum transferrin saturation (%)	29.1	5.3	29.4	5.7	0.83
Time to discharge (days)	10.2	1.8	10.5	2.1	0.68
Time to oral intake (days)	3.5	0.9	3.8	1.2	0.55
Time to ambulation (days)	2.1	0.6	2.3	0.8	0.42
Time to discharge (days)	10.2	1.8	10.5	2.1	0.68
Time to oral intake (days)	3.5	0.9	3.8	1.2	0.55
Time to ambulation (days)	2.1	0.6	2.3	0.8	0.42

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Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
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gac cca tca aaa gac ttg ata gct gaa ata cag aaa cag ggg gat gac 1008
Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Asp Asp
325 330 335

caa tgg aca tat caa att tac caa gaa cca ttc aaa aac ctg aag aca 1056
Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
340 345 350

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Gly Lys Tyr Ala Lys Arg Arg Thr Thr His Thr Asn Asp Val Lys Gln
355 360 365

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Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys
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<210> 16

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 16

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Lys	Ala	Leu	Thr	Ala	Ile	Cys	Glu	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile
		35					40					45			
Thr	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile
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Lys	Lys	Glu	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu
65					70					75					80

Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile
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Phe	Gln	Ala	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Ala	Lys	Asn
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Pro	Glu	Ile	Val	Ile	Tyr	Gln	His	Met	Ala	Ala	Leu	Tyr	Val	Gly	Ser
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Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	Arg	Glu
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His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys
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Thr	Val	Gln	Pro	Ile	Gln	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn
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Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Thr	Ser	Gln	Ile	Tyr
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Ala	Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr
305					310					315					320
Asp	Pro	Ser	Lys	Asp	Leu	Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Asp	Asp
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<211> 13584
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; Note =
        synthetic construct
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ggtaaagaaa	aaattaaaag	aacactacaa	taagacaata	gaatttaacc	caccctcagg	8640
aggggatcta	gaagttacaa	cacatagctt	taattgtaga	ggagaatttt	tctattgcaa	8700
tacaacaaaa	ctgttttcaa	acaacagtga	ttcaaacaac	gaaaccatca	cactcccatg	8760
caagataaaa	caaattataa	acatgtggga	gaaggtagga	cgagcaatgt	atgcccctcc	8820
cattgaagga	aacataaacat	gtaaatcaaa	tatcacagga	ctactattga	cacgtgatgg	8880
aggaaagaat	acaacaaatg	agatatttcag	accgggagga	ggaaaatga	aggacaattg	8940
gagaagtga	ttatataaat	ataaagtggg	agaaaattgag	ccattgggag	tagcaccac	9000
taaatcaaaa	aggagagtgg	tggagagaga	aaaaagagca	gtgggactag	gagctgtact	9060
ccttgggttc	ttgggagcag	caggaagcac	tatgggcgcg	gcgtcaataa	cgctgacggt	9120
acaggccaga	caactgttgt	ctggtatagt	gcaacagcaa	agcaatttgc	tgagagctat	9180
agaggcgcaa	cagcatatgt	tgcaactcac	ggtctggggc	attaagcagc	tccagacaag	9240
agtcttggct	atagagagat	acctaaagga	tcaacagctc	ctagggcttt	ggggctgctc	9300
tggaaaaatc	atctgcacca	ctgctgtgcc	ttggaactcc	agttggagta	ataaatctca	9360
agaagatatt	tgggataaca	tgacctggat	gcagtgggat	agagaaatta	gtaattacac	9420
aggcacaata	tataggttac	ttgaagactc	gcaaaaccag	caggagaaaa	atgaaaaaga	9480
tttattagca	ttggacagtt	ggaaaaactt	gtggaattgg	tttaacataa	caaattggct	9540
gtggtatata	aaaatattca	tcatgatagt	aggaggcttg	ataggtttga	gaataatttt	9600
tggtgtactc	gctatagtga	aaagagttag	gcagggatac	tcacctttgt	cgtttcagac	9660
ccttacccca	agcccagggg	gtcccagacag	gctcgaaga	atcgaagaag	aagggtggaga	9720
gcaagacaaa	gacagatcca	ttcgattagt	gagcggattc	ttagcacttg	cctgggacga	9780
tctgcggagc	ctgtgcctct	tcagctacca	ccacttgaga	gacttcatat	tgattgcagc	9840
gagagcagcg	gaacttctgg	gacgcagcag	tctcagggga	ctgcagagag	gggtgggaagc	9900
ccttaagtat	ctgggaaatc	ttgtgcagta	tgggggtctg	gagctaaaaa	gaagtgtctat	9960
taaactgttt	gataccatag	caatagcagt	agctgaagga	acagatagga	ttcttgaagt	10020
aatacagaga	atttgtagag	ctatccgcca	catacctata	agaataagac	agggccttga	10080
agcagctttg	caataattaa	ttaagtaacc	gatacagcag	caattggcaa	gctgcttaca	10140
tagaactcgc	ggcgattggc	atgccgcctt	aaaattttta	ttttattttt	tcttttcttt	10200

[illegible]

<210> 18
 <211> 2532
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
 synthetic construct

<221> CDS

<222> (1)...(2532)

<400> 18

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Met Arg Val Met Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp	
1 5 10 15	
ggc acc tta ggc ttt tgg atg ata ata att tgt agg gtg gtg ggg aac	96
Gly Thr Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Val Gly Asn	
20 25 30	
ttg aac ttg tgg gtc aca gtc tat tat ggg gta cct gtg tgg aaa gaa	144
Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu	
35 40 45	
gca aaa act act cta ttc tgt gca tca gat gct aaa gca tat gat aaa	192
Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys	
50 55 60	
gaa gta cat aat gtc tgg gct aca cat gcc tgt gta ccc aca gac ccc	240
Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro	
65 70 75 80	
aac cca cga gaa ata gtt ttg gaa aat gta aca gaa aat ttt aac atg	288
Asn Pro Arg Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met	
85 90 95	
tgg aaa aat gac atg gtg gat cag atg cat gag gat ata atc agt tta	336
Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu	
100 105 110	
tgg gat caa agc cta aaa cca tgt gta aag ttg acc cca ctc tgt gtc	384
Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val	
115 120 125	
act tta aat tgt aca aat gca cct gcc tac aat aat agc atg cat gga	432
Thr Leu Asn Cys Thr Asn Ala Pro Ala Tyr Asn Asn Ser Met His Gly	
130 135 140	
gaa atg aaa aat tgc tct ttc aat aca acc aca gag ata aga gat agg	480
Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg Asp Arg	
145 150 155 160	
aaa cag aaa gcg tat gca ctt ttt tat aaa cct gat gta gtg cca ctt	528
Lys Gln Lys Ala Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu	
165 170 175	

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aat	agg	aga	gaa	gag	aat	aat	ggg	aca	gga	gag	tat	ata	tta	ata	aat	576
Asn	Arg	Arg	Glu	Glu	Asn	Asn	Gly	Thr	Gly	Glu	Tyr	Ile	Leu	Ile	Asn	
			180					185					190			
tgc	aat	tcc	tca	acc	ata	aca	caa	gcc	tgt	cca	aag	gtc	act	ttt	gac	624
Cys	Asn	Ser	Ser	Thr	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Thr	Phe	Asp	
			195				200					205				
cca	att	cct	ata	cat	tat	tgt	gct	cca	gct	ggg	tat	gcg	att	cta	aag	672
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	
			210			215					220					
tgt	aat	aat	aag	aca	ttc	aat	ggg	aca	gga	cca	tgc	aat	aat	gtc	agc	720
Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	
					230					235					240	
aca	gta	caa	tgt	aca	cat	gga	att	atg	cca	gtg	gta	tca	act	caa	tta	768
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Met	Pro	Val	Val	Ser	Thr	Gln	Leu	
				245					250					255		
ctg	tta	aat	ggg	agc	cta	gca	gaa	gaa	gag	ata	ata	att	aga	tct	gaa	816
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	
			260				265					270				
aat	ctg	aca	aac	aat	atc	aaa	aca	ata	ata	gtc	cac	ctt	aat	aaa	tct	864
Asn	Leu	Thr	Asn	Asn	Ile	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Lys	Ser	
			275			280						285				
gta	gaa	att	gtg	tgt	aca	aga	ccc	aac	aat	aat	aca	aga	aaa	agt	ata	912
Val	Glu	Ile	Val	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	
			290			295					300					
agg	ata	gga	cca	gga	caa	aca	ttc	tat	gca	aca	ggg	gaa	ata	ata	gga	960
Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	
					310					315					320	
aac	ata	aga	gaa	gca	cat	tgt	aac	att	agt	aaa	agt	aac	tgg	acc	agt	1008
Asn	Ile	Arg	Glu	Ala	His	Cys	Asn	Ile	Ser	Lys	Ser	Asn	Trp	Thr	Ser	
				325					330					335		
act	tta	gaa	cag	gta	aag	aaa	aaa	tta	aaa	gaa	cac	tac	aat	aag	aca	1056
Thr	Leu	Glu	Gln	Val	Lys	Lys	Lys	Leu	Lys	Glu	His	Tyr	Asn	Lys	Thr	
			340					345					350			
ata	gaa	ttt	aac	cca	ccc	tca	gga	ggg	gat	cta	gaa	gtt	aca	aca	cat	1104
Ile	Glu	Phe	Asn	Pro	Pro	Ser	Gly	Gly	Asp	Leu	Glu	Val	Thr	Thr	His	
			355				360					365				
agc	ttt	aat	tgt	aga	gga	gaa	ttt	ttc	tat	tgc	aat	aca	aca	aaa	ctg	1152
Ser	Phe	Asn	Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Thr	Lys	Leu	
			370			375					380					
ttt	tca	aac	aac	agt	gat	tca	aac	aac	gaa	acc	atc	aca	ctc	cca	tgc	1200

aag ata aaa caa att ata aac atg tgg cag aag gta gga cga gca atg Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met 405 410 415	1248
tat gcc cct ccc att gaa gga aac ata aca tgt aaa tca aat atc aca Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr 420 425 430	1296
gga cta cta ttg aca cgt gat gga gga aag aat aca aca aat gag ata Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile 435 440 445	1344
ttc aga ccg gga gga gga aat atg aag gac aat tgg aga agt gaa tta Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu 450 455 460	1392
tat aaa tat aaa gtg gta gaa att gag cca ttg gga gta gca ccc act Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr 465 470 475 480	1440
aaa tca aaa agg aga gtg gtg gag aga gaa aaa aga gca gtg gga cta Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu 485 490 495	1488
gga gct gta ctc ctt ggg ttc ttg gga gca gca gga agc act atg ggc Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly 500 505 510	1536
gcg gcg tca ata acg ctg acg gta cag gcc aga caa ctg ttg tct ggt Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly 515 520 525	1584
ata gtg caa cag caa agc aat ttg ctg aga gct ata gag gcg caa cag Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln 530 535 540	1632
cat atg ttg caa ctc acg gtc tgg ggc att aag cag ctc cag aca aga His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg 545 550 555 560	1680
gtc ttg gct ata gag aga tac cta aag gat caa cag ctc cta ggg ctt Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu 565 570 575	1728
tgg ggc tgc tct gga aaa atc atc tgc acc act gct gtg cct tgg aac Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn 580 585 590	1776
tcc agt tgg agt aat aaa tct caa gaa gat att tgg gat aac atg acc Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr 595 600 605	1824
tgg atg cag tgg gat aga gaa att agt aat tac aca ggc aca ata tat Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr 610 615 620	1872

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agg tta ctt gaa gac tcg caa aac cag cag gag aaa aat gaa aaa gat	1920
Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp	
625 630 635 640	
tta tta gca ttg gac agt tgg aaa aac ttg tgg aat tgg ttt aac ata	1968
Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile	
645 650 655	
aca aat tgg ctg tgg tat ata aaa ata ttc atc atg ata gta gga ggc	2016
Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly	
660 665 670	
ttg ata ggt ttg aga ata att ttt ggt gta ctc gct ata gtg aaa aga	2064
Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg	
675 680 685	
gtt agg cag gga tac tca cct ttg tcg ttt cag acc ctt acc cca agc	2112
Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser	
690 695 700	
ccg agg ggt ccc gac agg ctc gga aga atc gaa gaa gaa ggt gga gag	2160
Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu	
705 710 715 720	
caa gac aaa gac aga tcc att cga tta gtg agc gga ttc tta gca ctt	2208
Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu	
725 730 735	
gcc tgg gac gat ctg cgg agc ctg tgc ctc ttc agc tac cac cac ttg	2256
Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu	
740 745 750	
aga gac ttc ata ttg att gca gcg aga gca gcg gaa ctt ctg gga cgc	2304
Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg	
755 760 765	
agc agt ctc agg gga ctg cag aga ggg tgg gaa gcc ctt aag tat ctg	2352
Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu	
770 775 780	
gga aat ctt gtg cag tat ggg ggt ctg gag cta aaa aga agt gct att	2400
Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile	
785 790 795 800	
aaa ctg ttt gat acc ata gca ata gca gta gct gaa gga aca gat agg	2448
Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg	
805 810 815	
att ctt gaa gta ata cag aga att tgt aga gct atc cgc cac ata cct	2496
Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro	
820 825 830	
ata aga ata aga cag ggc ttt gaa gca gct ttg caa	2532
Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln	
835 840	

<213> Artificial Sequence

<223> Description of Artificial Sequence; Note =
synthetic construct

Met 1	Arg	Val	Met	Gly 5	Ile	Gln	Arg	Asn	Trp 10	Pro	Gln	Trp	Trp	Ile 15	Trp
Gly	Thr	Leu	Gly	Phe	Trp	Met	Ile	Ile	Ile	Cys	Arg	Val	Val	Gly	Asn
			20					25				30			
Leu	Asn	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu
		35					40				45				
Ala	Lys	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Lys
	50					55				60					
Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro
65				70					75					80	
Asn	Pro	Arg	Glu	Ile	Val	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met
			85					90					95		
Trp	Lys	Asn	Asp	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu
			100				105					110			
Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val
		115					120				125				
Thr	Leu	Asn	Cys	Thr	Asn	Ala	Pro	Ala	Tyr	Asn	Asn	Ser	Met	His	Gly
	130					135				140					
Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Thr	Thr	Thr	Glu	Ile	Arg	Asp	Arg
145				150					155					160	
Lys	Gln	Lys	Ala	Tyr	Ala	Leu	Phe	Tyr	Lys	Pro	Asp	Val	Val	Pro	Leu
			165					170						175	
Asn	Arg	Arg	Glu	Glu	Asn	Asn	Gly	Thr	Gly	Glu	Tyr	Ile	Leu	Ile	Asn
			180				185					190			
Cys	Asn	Ser	Ser	Thr	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Thr	Phe	Asp
		195					200				205				
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys
	210					215				220					
Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser
225				230					235					240	
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Met	Pro	Val	Val	Ser	Thr	Gln	Leu
			245					250					255		
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu
		260					265					270			
Asn	Leu	Thr	Asn	Asn	Ile	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Lys	Ser
		275					280				285				
Val	Glu	Ile	Val	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile
	290					295					300				
Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly
305				310					315						320
Asn	Ile	Arg	Glu	Ala	His	Cys	Asn	Ile	Ser	Lys	Ser	Asn	Trp	Thr	Ser
			325					330					335		
Thr	Leu	Glu	Gln	Val	Lys	Lys	Lys	Leu	Lys	Glu	His	Tyr	Asn	Lys	Thr
		340					345					350			
Ile	Glu	Phe	Asn	Pro											

Parameter	Unit	Value	Standard Error	t-Statistic	p-Value
Intercept		0.0000	0.0000	0.0000	0.0000
Age	Years	0.0000	0.0000	0.0000	0.0000
Age squared	Years squared	0.0000	0.0000	0.0000	0.0000
Age cubed	Years cubed	0.0000	0.0000	0.0000	0.0000
Age quart	Years quart	0.0000	0.0000	0.0000	0.0000
Age quint	Years quint	0.0000	0.0000	0.0000	0.0000
Age sext	Years sext	0.0000	0.0000	0.0000	0.0000
Age sept	Years sept	0.0000	0.0000	0.0000	0.0000
Age oct	Years oct	0.0000	0.0000	0.0000	0.0000
Age non	Years non	0.0000	0.0000	0.0000	0.0000
Age dec	Years dec	0.0000	0.0000	0.0000	0.0000
Age ele	Years ele	0.0000	0.0000	0.0000	0.0000
Age twel	Years twel	0.0000	0.0000	0.0000	0.0000
Age thir	Years thir	0.0000	0.0000	0.0000	0.0000
Age four	Years four	0.0000	0.0000	0.0000	0.0000
Age five	Years five	0.0000	0.0000	0.0000	0.0000
Age six	Years six	0.0000	0.0000	0.0000	0.0000
Age sev	Years sev	0.0000	0.0000	0.0000	0.0000
Age eigh	Years eigh	0.0000	0.0000	0.0000	0.0000
Age nine	Years nine	0.0000	0.0000	0.0000	0.0000
Age ten	Years ten	0.0000	0.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	0.0000
Age twel	Years twel	0.0000	0.0000	0.0000	0.0000
Age thir	Years thir	0.0000	0.0000	0.0000	0.0000
Age four	Years four	0.0000	0.0000	0.0000	0.0000
Age five	Years five	0.0000	0.0000	0.0000	0.0000
Age six	Years six	0.0000	0.0000	0.0000	0.0000
Age sev	Years sev	0.0000	0.0000	0.0000	0.0000
Age eigh	Years eigh	0.0000	0.0000	0.0000	0.0000
Age nine	Years nine	0.0000	0.0000	0.0000	0.0000
Age ten	Years ten	0.0000	0.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	0.0000
Age twel	Years twel	0.0000	0.0000	0.0000	0.0000
Age thir	Years thir	0.0000	0.0000	0.0000	0.0000
Age four	Years four	0.0000	0.0000	0.0000	0.0000
Age five	Years five	0.0000	0.0000	0.0000	0.0000
Age six	Years six	0.0000	0.0000	0.0000	0.0000
Age sev	Years sev	0.0000	0.0000	0.0000	0.0000
Age eigh	Years eigh	0.0000	0.0000	0.0000	0.0000
Age nine	Years nine	0.0000	0.0000	0.0000	0.0000
Age ten	Years ten	0.0000	0.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	0.0000
Age twel	Years twel	0.0000	0.0000	0.0000	0.0000
Age thir	Years thir	0.0000	0.0000	0.0000	0.0000
Age four	Years four	0.0000	0.0000	0.0000	0.0000
Age five	Years five	0.0000	0.0000	0.0000	0.0000
Age six	Years six	0.0000	0.0000	0.0000	0.0000
Age sev	Years sev	0.0000	0.0000	0.0000	0.0000
Age eigh	Years eigh	0.0000	0.0000	0.0000	0.0000
Age nine	Years nine	0.0000	0.0000	0.0000	0.0000
Age ten	Years ten	0.0000	0.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	0.0000
Age twel	Years twel	0.0000	0.0000	0.0000	0.0000
Age thir	Years thir	0.0000	0.0000	0.0000	0.0000
Age four	Years four	0.0000	0.0000	0.0000	0.0000
Age five	Years five	0.0000	0.0000	0.0000	0.0000
Age six	Years six	0.0000			

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ATTORNEY DOCKET NO. 01113.0001U3

Ile	Leu	Glu	Val	Ile	Gln	Arg	Ile	Cys	Arg	Ala	Ile	Arg	His	Ile	Pro
			820					825					830		
Ile	Arg	Ile	Arg	Gln	Gly	Phe	Glu	Ala	Ala	Leu	Gln				
		835					840								

01113.0001U3